

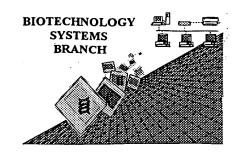
### **PCT OPERATIONS**

### FACSIMILE TRANSMISSION COVER SHEET

TELEPHO	NE:
FAX NO.:	703 243-6410
FROM: Barli	ara
TELEPHON	NE: <u>703 305 3831</u>
FAX NO.:	703-308-4785 OR 703-305-3230
MESSAGE:	-

BC

# RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/673,400

Source: PCT-09

Date Processed by STIC:  $\frac{1/23/2001}{2001}$ 

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail hclp: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail hclp: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

#### Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

### Raw Sequence Listing Error Summary

#### SERIAL NUMBER: ERROR DETECTED SUGGESTED CORRECTION ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE The number/text at the end of each line "wrapped" down to the next line. Wrapped Nucleics This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". The amino acid number/text at the end of each line "wrapped" down to the next line. Wrapped Aminos This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". The rules require that a line not exceed 72 characters in length. This includes spaces. Incorrect Line Length The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs Misaligned Amino Acid between the numbering. It is recommended to delete any tabs and use spacing between the numbers. This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Non-ASCII Please ensure your subsequent submission is saved in ASCII text so that it can be processed. Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue. Variable Length As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid Patentin ver. 2.0 "bug" Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. missing. If intentional, please use the following format for each skipped sequence: Sequence(s) \_ Skipped Sequences (2) INFORMATION FOR SEQ ID NO:X: (OLD RULES) (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence. Skipped Sequences <210> sequence id number (NEW RULES) <400> sequence id number 000 Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of n's or Xaa's Use of <220> to <223> is MANDATORY if n's or Xaa's are present. (NEW RULES) In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response. Use of <213>Organism (NEW RULES) are missing the <220>Feature and associated headings. Use of <220>Feature Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" (NEW RULES) Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted Patentin ver. 2.0 "bug" file, Tesalting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

Instead, please use "File Manager" or any other means to copy file to floppy disk.

1 AGE:

#### RAW SEQUENCE LISTING

PATENT APPLICATION US/09/673,400

DATE: 01/23/2001

TIME: 10:54:59

Input Set: I673400.RAW

This Raw Listing contains the General

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Corrected Diskette Needed

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(110> metagen Gesellschaft f?r Genomforschung mbH

(120> Menschliche Nukleinsureseguenzen 2007)

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the CRF program

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RRORED SEQUENCES FOLLOW

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## RAW SEQUENCE LISTING PATENT APPLICATION US/09/673,400

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VERIFICATION SUMMARY DATE: 01/23/2001
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